RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _____ 10/591,419 _____

Source: _____ IFWP _____

Date Processed by STIC: _____ 09/13/2006

ENTERED

RAW SEQUENCE LISTING   DATE: 09/13/2006
PATENT APPLICATION: US/10/591,419   TIME: 13:09:30

Input Set : **N:\RJAVED\10591419.txt**
Output Set: **N:\CRF4\09132006\J591419.raw**

```
 3 <110> APPLICANT: Frohberg, Claus
 4        Koetting, Oliver
 5        Ritte, Gerhard
 6        Steup, Martin
 8 <120> TITLE OF INVENTION: Methods for identifying proteins with starch phosphorylating
enzymatic
 9        activity
11 <130> FILE REFERENCE: 65084.000020
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C--> `13 <140> CURRENT APPLICATION NUMBER: US/10/591,419`

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14 <141> CURRENT FILING DATE: 2006-09-01
16 <150> PRIOR APPLICATION NUMBER: PCT/EP2005/002454
17 <151> PRIOR FILING DATE: 2005-03-04
19 <150> PRIOR APPLICATION NUMBER: EP04090483.1
20 <151> PRIOR FILING DATE: 2004-12-15
22 <150> PRIOR APPLICATION NUMBER: EP04090121.7
23 <151> PRIOR FILING DATE: 2004-03-29
25 <150> PRIOR APPLICATION NUMBER: EP04090087.0
26 <151> PRIOR FILING DATE: 2004-03-05
28 <150> PRIOR APPLICATION NUMBER: US60/549,980 provisional
29 <151> PRIOR FILING DATE: 2004-03-05
31 <160> NUMBER OF SEQ ID NOS: 46
33 <170> SOFTWARE: PatentIn version 3.1
35 <210> SEQ ID NO: 1
36 <211> LENGTH: 3591
37 <212> TYPE: DNA
38 <213> ORGANISM: Arabidopsis thaliana
40 <220> FEATURE:
41 <221> NAME/KEY: CDS
42 <222> LOCATION: (1)..(3591)
43 <223> OTHER INFORMATION:
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W--> `46 <400> 1`

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47 atg gag agc att ggc agc cat tgt tgc agc tct cct ttc acc ttc atc        48
48 Met Glu Ser Ile Gly Ser His Cys Cys Ser Ser Pro Phe Thr Phe Ile
49 1               5                   10                  15
51 act aga aac tca tca tca tca ctt cct aga ctc gtt aac atc act cac        96
52 Thr Arg Asn Ser Ser Ser Ser Leu Pro Arg Leu Val Asn Ile Thr His
53              20                  25                  30
55 aga gtt aat ctc agc cac caa tct cac cga ctc aga aac tcc aat tct       144
56 Arg Val Asn Leu Ser His Gln Ser His Arg Leu Arg Asn Ser Asn Ser
57          35                  40                  45
59 cgt ctc act tgc act gct act tct tct tcc acc att gag gaa caa cgg       192
60 Arg Leu Thr Cys Thr Ala Thr Ser Ser Ser Thr Ile Glu Glu Gln Arg
61      50                  55                  60
63 aag aag aaa gat gga tca gga acg aaa gtg agg ttg aat gtg agg tta       240
```

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64  Lys Lys Lys Asp Gly Ser Gly Thr Lys Val Arg Leu Asn Val Arg Leu
65  65              70              75              80
67  gat cat caa gtt aat ttt ggt gac cat gtg gct atg ttt gga tca gct   288
68  Asp His Gln Val Asn Phe Gly Asp His Val Ala Met Phe Gly Ser Ala
69              85              90              95
71  aaa gag att ggt tca tgg aaa aag aaa tcg cct ttg aat tgg agt gag   336
72  Lys Glu Ile Gly Ser Trp Lys Lys Lys Ser Pro Leu Asn Trp Ser Glu
73              100             105             110
75  aat gga tgg gtt tgt gag ttg gaa ctt gac ggt ggt cag gtt ttg gag   384
76  Asn Gly Trp Val Cys Glu Leu Glu Leu Asp Gly Gly Gln Val Leu Glu
77              115             120             125
79  tat aag ttt gtc att gtt aag aat gat ggt tca ctt tca tgg gaa tct   432
80  Tyr Lys Phe Val Ile Val Lys Asn Asp Gly Ser Leu Ser Trp Glu Ser
81      130             135             140
83  ggt gat aat cgt gtc ctt aag gtt cca aat tct ggg aat ttt tct gtt   480
84  Gly Asp Asn Arg Val Leu Lys Val Pro Asn Ser Gly Asn Phe Ser Val
85  145             150             155             160
87  gtt tgt cat tgg gat gct act aga gaa acc ctt gat ttg cct cag gag   528
88  Val Cys His Trp Asp Ala Thr Arg Glu Thr Leu Asp Leu Pro Gln Glu
89              165             170             175
91  gtt ggt aat gat gat gat gtt ggt gat ggt ggg cat gag agg gat aat   576
92  Val Gly Asn Asp Asp Asp Val Gly Asp Gly Gly His Glu Arg Asp Asn
93              180             185             190
95  cat gat gtt ggt gat gat aga gta gtg gga agt gaa aat ggt gcg cag   624
96  His Asp Val Gly Asp Asp Arg Val Val Gly Ser Glu Asn Gly Ala Gln
97      195             200             205
99  ctt cag aag agt aca ttg ggt ggg caa tgg caa ggt aaa gat gcg tcc   672
100 Leu Gln Lys Ser Thr Leu Gly Gly Gln Trp Gln Gly Lys Asp Ala Ser
101     210             215             220
103 ttt atg cgt tct aat gat cat ggt aac aga gaa gtt ggt aga aat tgg   720
104 Phe Met Arg Ser Asn Asp His Gly Asn Arg Glu Val Gly Arg Asn Trp
105 225             230             235             240
107 gat act agt ggt ctt gaa ggc aca gct ctt aag atg gtt gag ggt gat   768
108 Asp Thr Ser Gly Leu Glu Gly Thr Ala Leu Lys Met Val Glu Gly Asp
109             245             250             255
111 cgc aac tct aag aac tgg tgg aga aag ctt gaa atg gta cgc gag gtt   816
112 Arg Asn Ser Lys Asn Trp Trp Arg Lys Leu Glu Met Val Arg Glu Val
113             260             265             270
115 ata gtt ggg agt gtt gag agg gag gaa cga ttg aag gcg ctc ata tac   864
116 Ile Val Gly Ser Val Glu Arg Glu Glu Arg Leu Lys Ala Leu Ile Tyr
117             275             280             285
119 tct gca att tat ttg aag tgg ata aac aca ggt cag att cct tgt ttt   912
120 Ser Ala Ile Tyr Leu Lys Trp Ile Asn Thr Gly Gln Ile Pro Cys Phe
121     290             295             300
123 gaa gat gga ggg cat cac cgt cca aac agg cat gcc gag att tcc aga   960
124 Glu Asp Gly Gly His His Arg Pro Asn Arg His Ala Glu Ile Ser Arg
125 305             310             315             320
127 ctt ata ttc cgt gag ttg gag cac att tgc agt aag aaa gat gct act  1008
128 Leu Ile Phe Arg Glu Leu Glu His Ile Cys Ser Lys Lys Asp Ala Thr
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129                   325                   330                   335
131 cca gag gaa gtg ctt gtt gct cgg aaa atc cat ccg tgt tta cct tct      1056
132 Pro Glu Glu Val Leu Val Ala Arg Lys Ile His Pro Cys Leu Pro Ser
133                   340                   345                   350
135 ttc aaa gca gag ttt act gca gct gtc cct cta act cgg att agg gac      1104
136 Phe Lys Ala Glu Phe Thr Ala Ala Val Pro Leu Thr Arg Ile Arg Asp
137           355                   360                   365
139 ata gcc cat cgg aat gat att cct cat gat ctc aag caa gaa atc aag      1152
140 Ile Ala His Arg Asn Asp Ile Pro His Asp Leu Lys Gln Glu Ile Lys
141       370                   375                   380
143 cat acg ata caa aat aag ctt cac cgg aat gct ggt cca gaa gat cta      1200
144 His Thr Ile Gln Asn Lys Leu His Arg Asn Ala Gly Pro Glu Asp Leu
145 385                   390                   395                   400
147 att gca aca gaa gca atg ctt caa cga att acc gag acc cca gga aaa      1248
148 Ile Ala Thr Glu Ala Met Leu Gln Arg Ile Thr Glu Thr Pro Gly Lys
149                   405                   410                   415
151 tat agt gga gac ttt gtg gag cag ttt aaa ata ttc cat aat gag ctt      1296
152 Tyr Ser Gly Asp Phe Val Glu Gln Phe Lys Ile Phe His Asn Glu Leu
153           420                   425                   430
155 aaa gat ttc ttt aat gct gga agt ctc act gaa cag ctt gat tct atg      1344
156 Lys Asp Phe Phe Asn Ala Gly Ser Leu Thr Glu Gln Leu Asp Ser Met
157           435                   440                   445
159 aaa att tct atg gat gat aga ggt ctt tct gcg ctc aat ttg ttt ttt      1392
160 Lys Ile Ser Met Asp Asp Arg Gly Leu Ser Ala Leu Asn Leu Phe Phe
161       450                   455                   460
163 gaa tgt aaa aag cgc ctt gac aca tca gga gaa tca agc aat gtt ttg      1440
164 Glu Cys Lys Lys Arg Leu Asp Thr Ser Gly Glu Ser Ser Asn Val Leu
165 465                   470                   475                   480
167 gag ttg att aaa acc atg cat tct cta gct tct tta aga gaa aca att      1488
168 Glu Leu Ile Lys Thr Met His Ser Leu Ala Ser Leu Arg Glu Thr Ile
169                   485                   490                   495
171 ata aag gaa ctt aat agc ggc ttg cga aat gat gct cct gat act gcc      1536
172 Ile Lys Glu Leu Asn Ser Gly Leu Arg Asn Asp Ala Pro Asp Thr Ala
173           500                   505                   510
175 att gca atg cgc cag aag tgg cgc ctt tgt gag atc ggc ctc gag gac      1584
176 Ile Ala Met Arg Gln Lys Trp Arg Leu Cys Glu Ile Gly Leu Glu Asp
177           515                   520                   525
179 tac ttt ttt gtt cta cta agc aga ttc ctc aat gct ctt gaa act atg      1632
180 Tyr Phe Phe Val Leu Leu Ser Arg Phe Leu Asn Ala Leu Glu Thr Met
181       530                   535                   540
183 gga gga gct gat caa ctg gca aaa gat gtg gga tca aga aac gtt gcc      1680
184 Gly Gly Ala Asp Gln Leu Ala Lys Asp Val Gly Ser Arg Asn Val Ala
185 545                   550                   555                   560
187 tca tgg aat gat cca cta gat gct ttg gtg ttg ggt gtt cac caa gta      1728
188 Ser Trp Asn Asp Pro Leu Asp Ala Leu Val Leu Gly Val His Gln Val
189                   565                   570                   575
191 ggt cta tct ggt tgg aag caa gaa gaa tgt tta gcc att gga aat gaa      1776
192 Gly Leu Ser Gly Trp Lys Gln Glu Glu Cys Leu Ala Ile Gly Asn Glu
193                   580                   585                   590
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195 ctc ctt gct tgg cga gaa agg gac cta ctt gaa aaa gaa ggg gaa gag    1824
196 Leu Leu Ala Trp Arg Glu Arg Asp Leu Leu Glu Lys Glu Gly Glu Glu
197         595                 600                 605
199 gat gga aaa aca att tgg gcc atg agg ctg aaa gca act ctt gat cga    1872
200 Asp Gly Lys Thr Ile Trp Ala Met Arg Leu Lys Ala Thr Leu Asp Arg
201         610                 615                 620
203 gca cgc aga tta aca gca gaa tat tct gat ttg ctt ctt caa ata ttt    1920
204 Ala Arg Arg Leu Thr Ala Glu Tyr Ser Asp Leu Leu Leu Gln Ile Phe
205 625                 630                 635                 640
207 cct cct aat gtg gag att tta gga aaa gct cta gga att cca gag aat    1968
208 Pro Pro Asn Val Glu Ile Leu Gly Lys Ala Leu Gly Ile Pro Glu Asn
209                 645                 650                 655
211 agt gtc aag acc tat aca gaa gca gag att cgt gct gga att att ttc    2016
212 Ser Val Lys Thr Tyr Thr Glu Ala Glu Ile Arg Ala Gly Ile Ile Phe
213         660                 665                 670
215 cag atc tca aag ctc tgc act gtt ctt cta aaa gct gta aga aat tca    2064
216 Gln Ile Ser Lys Leu Cys Thr Val Leu Leu Lys Ala Val Arg Asn Ser
217         675                 680                 685
219 ctt ggt tct gag ggc tgg gat gtc gtt gta cct gga tcg acg tct ggg    2112
220 Leu Gly Ser Glu Gly Trp Asp Val Val Val Pro Gly Ser Thr Ser Gly
221         690                 695                 700
223 aca tta gtt cag gtt gag agc att gtt ccg gga tca ttg cca gca act    2160
224 Thr Leu Val Gln Val Glu Ser Ile Val Pro Gly Ser Leu Pro Ala Thr
225 705                 710                 715                 720
227 tct ggt ggt cct att att ctc ttg gtc aat aaa gct gat ggc gat gaa    2208
228 Ser Gly Gly Pro Ile Ile Leu Leu Val Asn Lys Ala Asp Gly Asp Glu
229                 725                 730                 735
231 gag gta agt gct gct aat ggg aac ata gct gga gtc atg ctt ctg cag    2256
232 Glu Val Ser Ala Ala Asn Gly Asn Ile Ala Gly Val Met Leu Leu Gln
233         740                 745                 750
235 gag ctg cct cac ttg tct cac ctt ggc gtt aga gcg cgg cag gag aaa    2304
236 Glu Leu Pro His Leu Ser His Leu Gly Val Arg Ala Arg Gln Glu Lys
237         755                 760                 765
239 att gtc ttt gtg aca tgt gat gat gat gac aag gtt gct gat ata cga    2352
240 Ile Val Phe Val Thr Cys Asp Asp Asp Asp Lys Val Ala Asp Ile Arg
241         770                 775                 780
243 cga ctt gtg gga aaa ttt gtg agg ttg gaa gca tct cca agt cat gtg    2400
244 Arg Leu Val Gly Lys Phe Val Arg Leu Glu Ala Ser Pro Ser His Val
245 785                 790                 795                 800
247 aat ctg ata ctt tca act gag ggt agg agt cgc act tcc aaa tcc agt    2448
248 Asn Leu Ile Leu Ser Thr Glu Gly Arg Ser Arg Thr Ser Lys Ser Ser
249                 805                 810                 815
251 gcg acc aaa aaa acg gat aag aac agc tta tct aag aaa aaa aca gat    2496
252 Ala Thr Lys Lys Thr Asp Lys Asn Ser Leu Ser Lys Lys Lys Thr Asp
253         820                 825                 830
255 aag aag agc tta tct atc gat gat gaa gaa tca aag cct ggt tcc tca    2544
256 Lys Lys Ser Leu Ser Ile Asp Asp Glu Glu Ser Lys Pro Gly Ser Ser
257         835                 840                 845
259 tct tcc aat agc ctc ctt tac tct tcc aag gat atc cct agt gga gga    2592
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PATENT APPLICATION: US/10/591,419   TIME: 13:09:30

Input Set : **N:\RJAVED\10591419.txt**
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260 Ser Ser Asn Ser Leu Leu Tyr Ser Ser Lys Asp Ile Pro Ser Gly Gly
261     850                 855                 860
263 atc ata gca ctt gct gat gca gat gta cca act tct ggt tca aaa tct    2640
264 Ile Ile Ala Leu Ala Asp Ala Asp Val Pro Thr Ser Gly Ser Lys Ser
265 865                 870                 875                 880
267 gct gca tgt ggt ctt ctt gca tct tta gca gaa gcc tct agt aaa gtg    2688
268 Ala Ala Cys Gly Leu Leu Ala Ser Leu Ala Glu Ala Ser Ser Lys Val
269                 885                 890                 895
271 cac agc gaa cac gga gtt ccg gca tca ttt aag gtt cca act gga gtt    2736
272 His Ser Glu His Gly Val Pro Ala Ser Phe Lys Val Pro Thr Gly Val
273             900                 905                 910
275 gtc ata cct ttt gga tcg atg gaa tta gct tta aag caa aat aat tcg    2784
276 Val Ile Pro Phe Gly Ser Met Glu Leu Ala Leu Lys Gln Asn Asn Ser
277             915                 920                 925
279 gaa gaa aag ttt gcg tct ttg cta gaa aaa cta gaa acc gcc aga cct    2832
280 Glu Glu Lys Phe Ala Ser Leu Leu Glu Lys Leu Glu Thr Ala Arg Pro
281     930                 935                 940
283 gag ggt ggt gag cta gac gac ata tgt gac cag atc cat gaa gtg atg    2880
284 Glu Gly Gly Glu Leu Asp Asp Ile Cys Asp Gln Ile His Glu Val Met
285 945                 950                 955                 960
287 aaa acg ttg caa gtg cct aaa gaa aca atc aac agc ata agc aaa gcg    2928
288 Lys Thr Leu Gln Val Pro Lys Glu Thr Ile Asn Ser Ile Ser Lys Ala
289             965                 970                 975
291 ttt ctc aaa gat gct cgt ctc att gtt cgt tca agt gct aac gtc gag    2976
292 Phe Leu Lys Asp Ala Arg Leu Ile Val Arg Ser Ser Ala Asn Val Glu
293             980                 985                 990
295 gac tta gcc gga atg tca gct gca  gga ctc tat gaa tca  atc cct aac    3024
296 Asp Leu Ala Gly Met Ser Ala Ala  Gly Leu Tyr Glu Ser  Ile Pro Asn
297             995                 1000                1005
299 gtg agt  ccc tcg gat cct ttg  gtg ttt tca gat tcg  gtt tgc caa    3069
300 Val Ser  Pro Ser Asp Pro Leu  Val Phe Ser Asp Ser  Val Cys Gln
301     1010                1015                1020
303 gtt tgg  gct tct ctc tac aca  aga aga gct gtt cta  agc cgt aga    3114
304 Val Trp  Ala Ser Leu Tyr Thr  Arg Arg Ala Val Leu  Ser Arg Arg
305     1025                1030                1035
307 gct gct  ggt gtc tct caa aga  gaa gct tca atg gct  gtt ctc gtt    3159
308 Ala Ala  Gly Val Ser Gln Arg  Glu Ala Ser Met Ala  Val Leu Val
309     1040                1045                1050
311 caa gaa  atg ctt tcg ccg gac  tta tca ttc gtt ctg  cac aca gtg    3204
312 Gln Glu  Met Leu Ser Pro Asp  Leu Ser Phe Val Leu  His Thr Val
313     1055                1060                1065
315 agt cca  gct gat ccg gac agt  aac ctt gtg gaa gcc  gag atc gct    3249
316 Ser Pro  Ala Asp Pro Asp Ser  Asn Leu Val Glu Ala  Glu Ile Ala
317     1070                1075                1080
319 cct ggt  tta ggt gag act tta  gct tca gga aca aga  gga aca cca    3294
320 Pro Gly  Leu Gly Glu Thr Leu  Ala Ser Gly Thr Arg  Gly Thr Pro
321     1085                1090                1095
323 tgg aga  ctc gct tcg ggt aag  ctc gac ggg att gta  caa acc tta    3339
324 Trp Arg  Leu Ala Ser Gly Lys  Leu Asp Gly Ile Val  Gln Thr Leu
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VERIFICATION SUMMARY   DATE: 09/13/2006
PATENT APPLICATION: **US/10/591,419**   TIME: 13:09:31

Input Set : **N:\RJAVED\10591419.txt**
Output Set: **N:\CRF4\09132006\J591419.raw**

L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:46 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:43
L:674 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:671
L:1354 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:1351
L:1528 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:1525
L:1664 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:1661
L:1962 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:1959